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Input file Fbh2786c.seq; Output File 2786.trans
 Sequence length 2459

10	20	30	40	50	60	M	A	S	G	4	
GCGGCCGCGTCGACCTCCCTCGGGTTCCGCGCCCGCGCGGTGAGCAACGGCTCTGCGGCC	ATG	GCG	AGC	GGC						12	73
E H S P G S G A A R R P L H S A ¹⁶² A V D										24	
GAG CAT TCC CCC GGC AGC GGC GCG GCC CGG CGG CCG CTG CAC TCC GCG CAG GCT GTG GAC										72	133
V A S A S N F R A F E L L H L D L R										44	
GTG GCC TCG GCC TCC AAC TTC CGG GCC TTT GAG CTG CTG CAC TTG CAC CTG GAC CTG CGG										132	193
A E F G P P G P G A G S R G L S G T A V										64	
GCT GAG TTC GGG CCT CCA GGG CCC GGC GCA GGG AGC CGG GGG CTG AGC GGC ACC GCG GTC										192	253
L D L R C L E P E G A A E L R L D S H P										84	
CTG GAC CTG CGC TGC CTG GAG CCC GAG GGC GCC GCC GAG CTG CGG CTG GAC TCG CAC CCG										252	313
C L E V T A A A L R R E R P G S E E P P										104	
TGC CTG GAG GTG ACG GCG GCG GCG CTG CGG CGG GAG CGG CCC GGC TCG GAG GAG CCG CCT										312	373
A E P V S F Y T O P F S H Y G O A L C V										124	
GCG GAG CCC GTG AGC TTC TAC ACG CAG CCC TTC TCG CAC TAT GGC CAG GCC CTG TGC GTG										372	433
S F P O P C R A A E R L O V L L T Y R V										144	
TCC TTC CCG CAG CCC TGC CGC GCC GCC GAG CGC CTC CAG GTG CTG CTC ACC TAC CGC GTC										432	493
G E G P G V C W L A P E O T A G K K K P										164	
GGG GAG GGA CCC GGG GTT TGC TGG TTG GCT CCC GAG CAG ACA GCA GGA AAG AAG AAG CCC										492	553
F V Y T O G O A V L N R A F F P C F D T										184	
TTC GTG TAC ACC CAG GGC CAG GCT GTC CTA AAC CGG GCC TTC TTC CCT TGC TTC GAC ACG										552	613
P A V K Y K Y S A L I E V P D G F T A V										204	
CCT GCT GTT AAA TAC AAG TAT TCA GCT CTT ATT GAG GTC CCA GAT GGC TTC ACA GCT GTG										612	673
M S A S T W E K R G P N K F F F O M C O										224	
ATG AGT GCT AGC ACC TGG GAG AAG AGA GGT CCA AAT AAG TTC TTC CAG ATG TGT CAG										672	733
P I P S Y L I A L A I G D L V S A E V G										244	
CCC ATC CCC TCC TAT CTG ATA GCT TTG GCC ATC GGA GAT CTG GTT TCG GCT GAA GTT GGA										732	793
P R S R V W A E P C L I D A A N E E Y N										264	
CCC AGG AGC CGG GTG TGG GCT GAG CCC TGC CTG ATT GAT GCT GCC AAT GAG GAG TAC AAC										792	853
G V I E E F L A T G E K L F G P Y V W G										284	
GGG GTG ATA GAA GAA TTT TTG CCA ACA GGA GAG AAG CTT TTT GGA CCT TAT GTT TGG GGA										852	913
R Y D L L F M P P S F P F G G M E N P C										304	
AGG TAT GAC TTG CTC TFC ATG CCA CCG TCC TTT CCA TTT GGA GGA ATG GAG AAC CCT TGT										912	973
L T F V T P C L L A G D R S L A D V I I										324	
CTG ACC TTT GTC ACC CCC TGC CTG CTA GCT GGG GAG CGC TCC TTG GCA GAT GTC ATC ATC										972	1033
H E I S H S W F G N L V T N A N W G E F										344	
CAT GAG ATC TCC CAC AGT TGG TTT GGG AAC CTG GTC ACC AAC GCC AAC TGG GGT GAA TTC										1032	1093
W L N E G F T M Y A O R R I S T I L F G										364	
TGG CTC AAT GAA GGT TTC ACC ATG TAC GCC CAG AGG AGG ATC TCC ACC ATC CTC TTT GGC										1092	1153
A A Y T C L E A A T G R A L L R O H M D										384	
GCT GCG TAC ACC TGC TTG GAG GCT GCA ACG GGG CGG GCT CTG CTG CGT CAA CAC ATG GAC										1152	1213
I T G E E N P L N K L R V K I E P G V D										404	
ATC ACT GGA GAG GAA AAC CCA CTC AAC AAG CTC CGC GTG AAG ATT GAA CCA GGC GTT GAC										1212	1273
P D D T Y N E T P Y E K G F C F V S Y L										424	
CCG GAC GAC ACC TAT AAT GAG ACC CCC TAC GAG AAA GGT TTC TGC TTT GTC TCA TAC CTG										1272	1333
A H L V G D O D O F D S F L K A Y V H E										444	
GCC CAC TTG GTG GGT GAT CAG GAT CAG TTT GAC AGT TTT CTC AAG GCC TAT GTG CAT GAA										1332	1393
F K F R S I L A D D F L D F Y L E Y F P										464	
TTC AAA TTC CGA AGC ATC TTA GCC GAT GAC TTT CTG GAC TTC TAC TTG GAA TAT TTC CCT										1392	1453

FIG. 1A.

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E L K K K R V D I I P G F E F D R W L N 484
GAG CTT AAG AAA AAG AGA GTG GAT ATC ATT CCA GGT TTT GAG TTT GAT CGA TGG CTG AAT 1452 1513
T P G W P P Y L P D L S P G D S L M K P 504
ACC CCC GGC TGG CCC CCG TAC CTC CCT GAT CTC TCC CCT GGG GAC TCA CTC ATG AAG CCT 1512 1573
A E E L A Q L W A A E E L D M K A I E A 524
GCT GAA GAG CTA GCC CAA CTG TGG GCA GCC GAG GAG CTG GAC ATG AAG GCC ATT GAA GCC 1572 1633
V A I S P W K T Y O L V Y F L D K I L O 544
GTG GCC ATC TCT CCC TGG AAG ACC TAC CAG CTG GTC TAC TTC CTG GAT AAG ATC CTC CAG 1632 1693
K S P L P P G N V K K L G D T Y P S I S 564
AAA TCC CCT CTC CCT CCT GGG AAT GTG AAA AAA CTT GGA GAC ACA TAC CCA AGT ATC TCA 1692 1753
N A R N A E L R L R W G Q I V L K N D H 584
AAT GCC CGG AAT GCA GAG CTC CGG CTG CGA TGG GGC CAA ATC GTC CTT AAG AAC GAC CAC 1752 1813
O E D F W K V K E F L H N O G K Q K Y T 604
CAG GAA GAT TTC TGG AAA GTG AAG GAG TTC CTG CAT AAC CAG GGG AAG CAG AAG TAT ACA 1812 1873
L P L Y H A M M G G S E V A O T L A K E 624
CTT CCG CTG TAC CAC GCA ATG ATG GGT GGC AGT GAG GTG GCC CAG ACC CTC GCC AAG GAG 1872 1933
T F A S T A S O L H S N V V N Y V O O I 644
ACT TTT GCA TCC ACC GCC TCC CAG CTC CAC AGC AAT GTT GTC AAC TAT GTC CAG CAG ATC 1932 1993
V A P K G S * 651
GTG GCA CCC AAG GGC AGT TAG 1953
—2011
AGGCTCGTGTGCATGCCCTGCCTCTTCAGGCTCTCCAGGCTTTCAGAATAATTGTTTGTTCCTCCAAATTCCTGTTCCC
TGATCAACTTCCTGGAGTTTATATCCCCCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGACTCTTGGGCTCTGCTG
TCTGGTGGGAACCTTACTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCACAGCTCTCCCCGCTACAGGCT
GCAGGCACTGCAGGGCAGCGGGTATTCTCTCCCCACCTAAGTCTCTGGGAAGAAGTGGAGAGGACTGATGCTCTTCTT
TTTTCTCTTTCTGTCTTTTCTTGTGATTTTATGCAAAGGGCTGGCATTCTGATTGTTCTTTTTCAGGTTTAAATCC
TTATTTTAATAAAGTTTCAAGCAAAATTAATAAAAAAAAAAAAAAAAAAAAA

FIG. 1B.

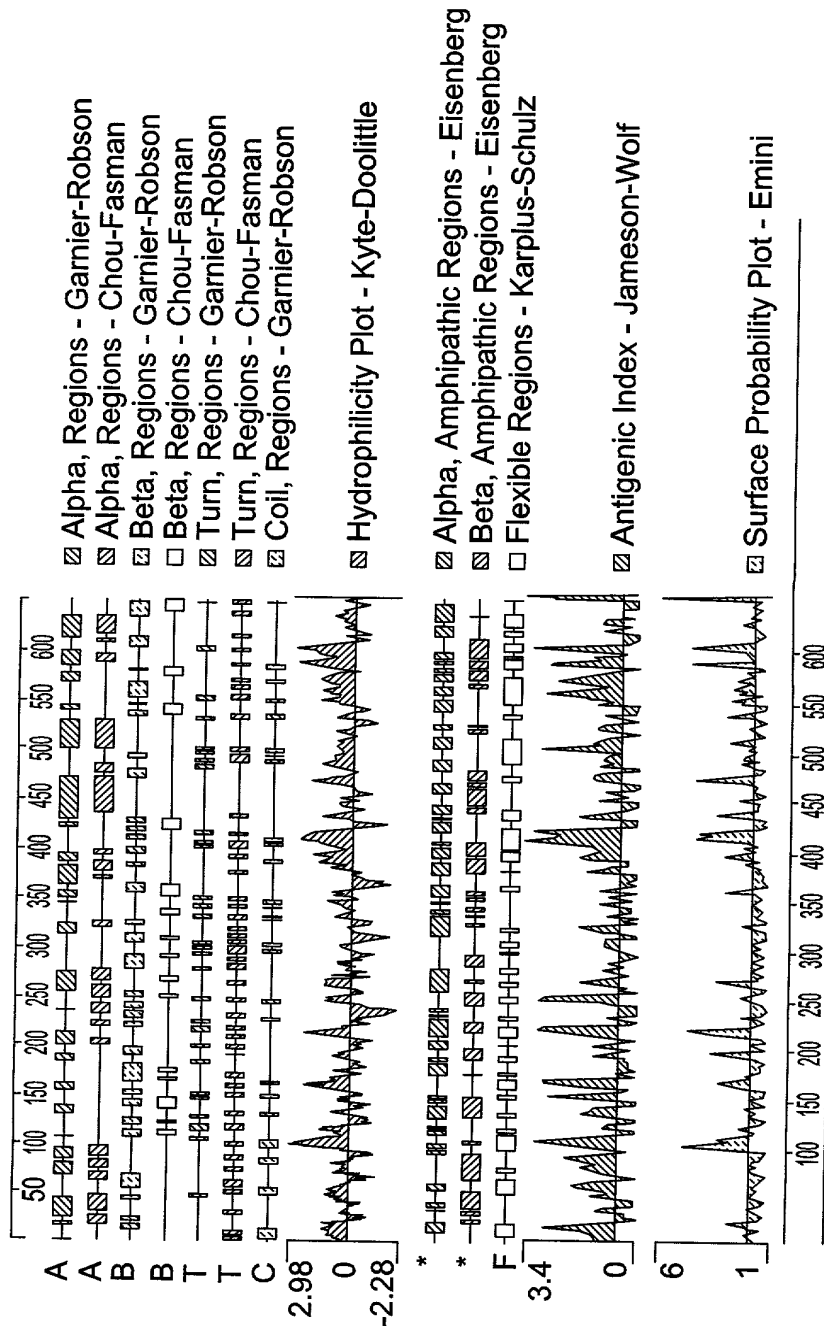


FIG. 2.

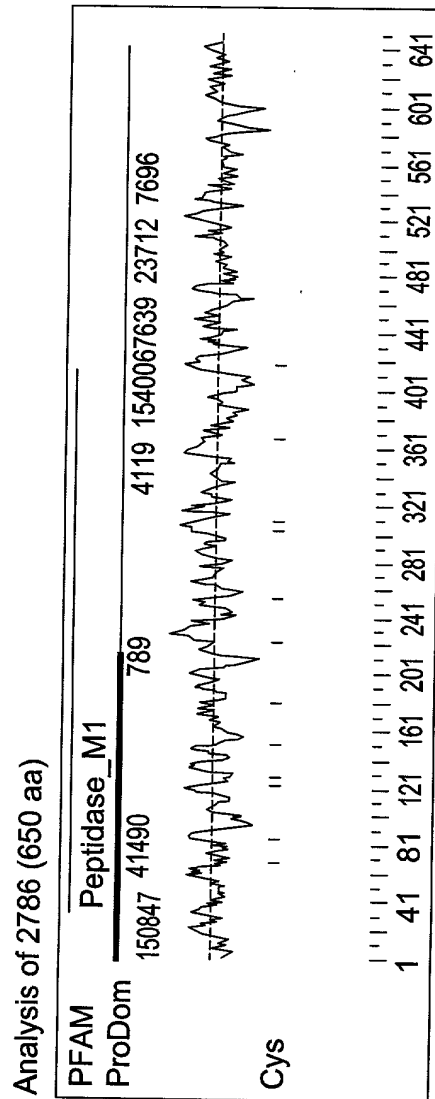


FIG. 3.

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Prosite Pattern Matches for 2786

Prosite version: Release 12.2 of February 1995

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 356 RRIS 359

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 141 TYR 143

Query: 374 TGR 376

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 208 STWE 211

Analysis of 2786

Query: 318 SLAD 321

Query: 368 TCLE 371

Query: 386 TGEE 389

Query: 408 TYNE 411

Query: 412 TPYE 415

Query: 496 SPGD 499

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 9 GSGAAR 14

Query: 58 GLSGTA 63

Query: 119 GQALCV 124

Query: 333 GNLVTN 338

Query: 364 GAAYTC 369

Query: 614 GSEVAQ 619

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 159 AGKK 162

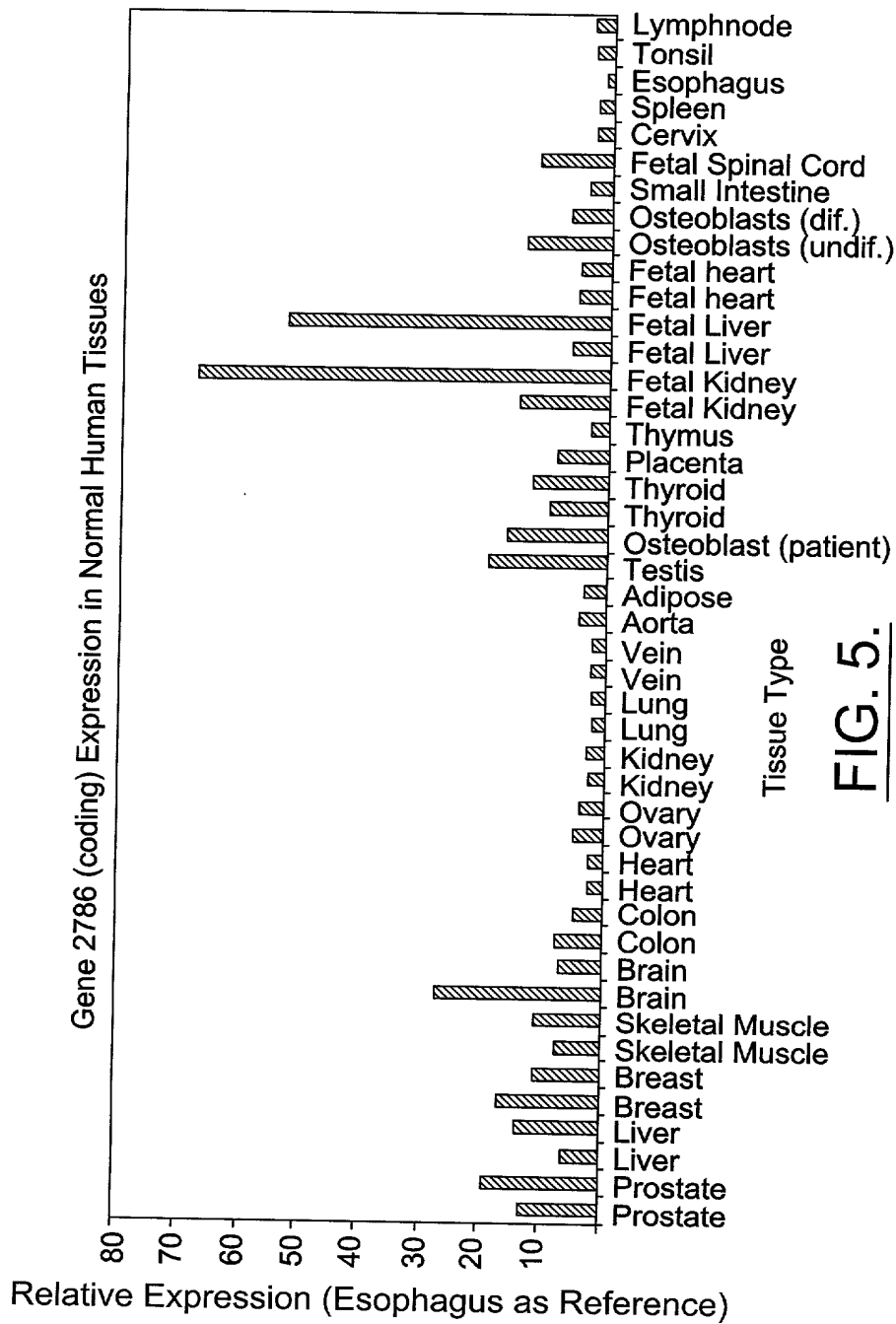
>PS00030/PDOC00030/RNP_1 Eukaryotic putative RNA-binding region RNP-1 signature.

Query: 416 KGFCFVS 423

>PS00142/PDOC00129/ZINC_PROTEASE Neutral zinc metalloproteases, zinc-binding region signature.

Query: 322 VIIHEISHSW 331

FIG. 4.



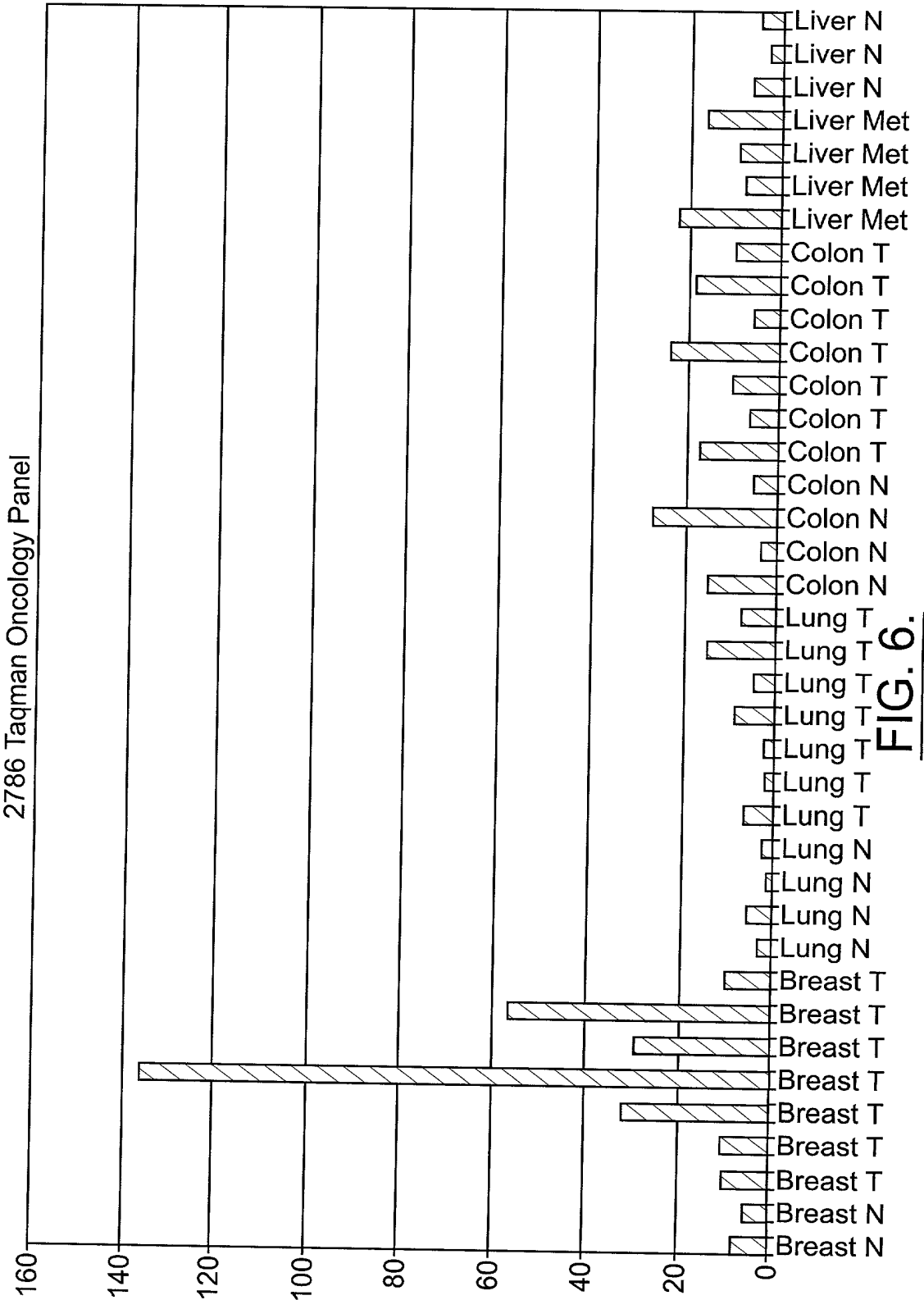


FIG. 6.

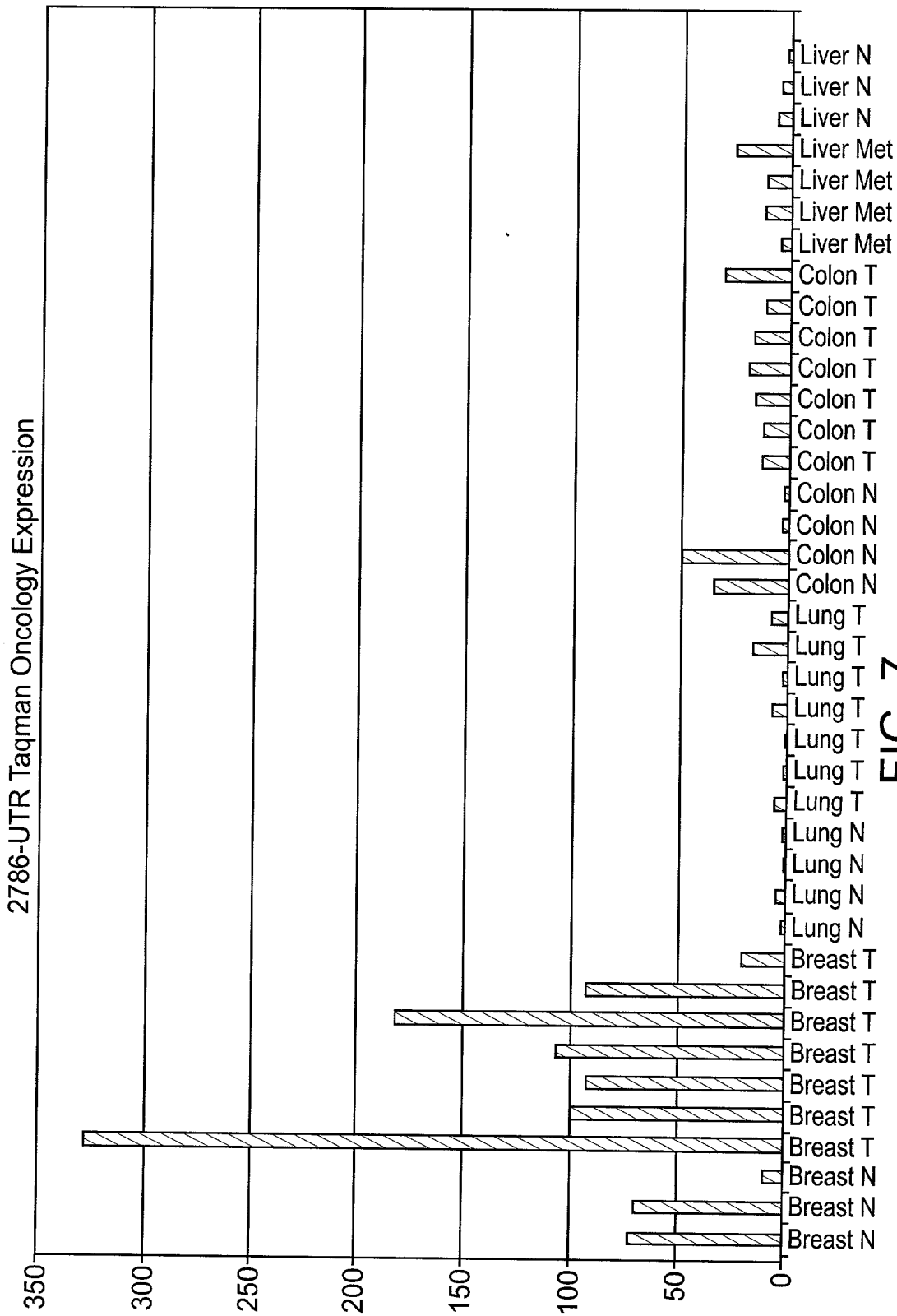


FIG. 7.

2786 Expression in Normal Human Tissue

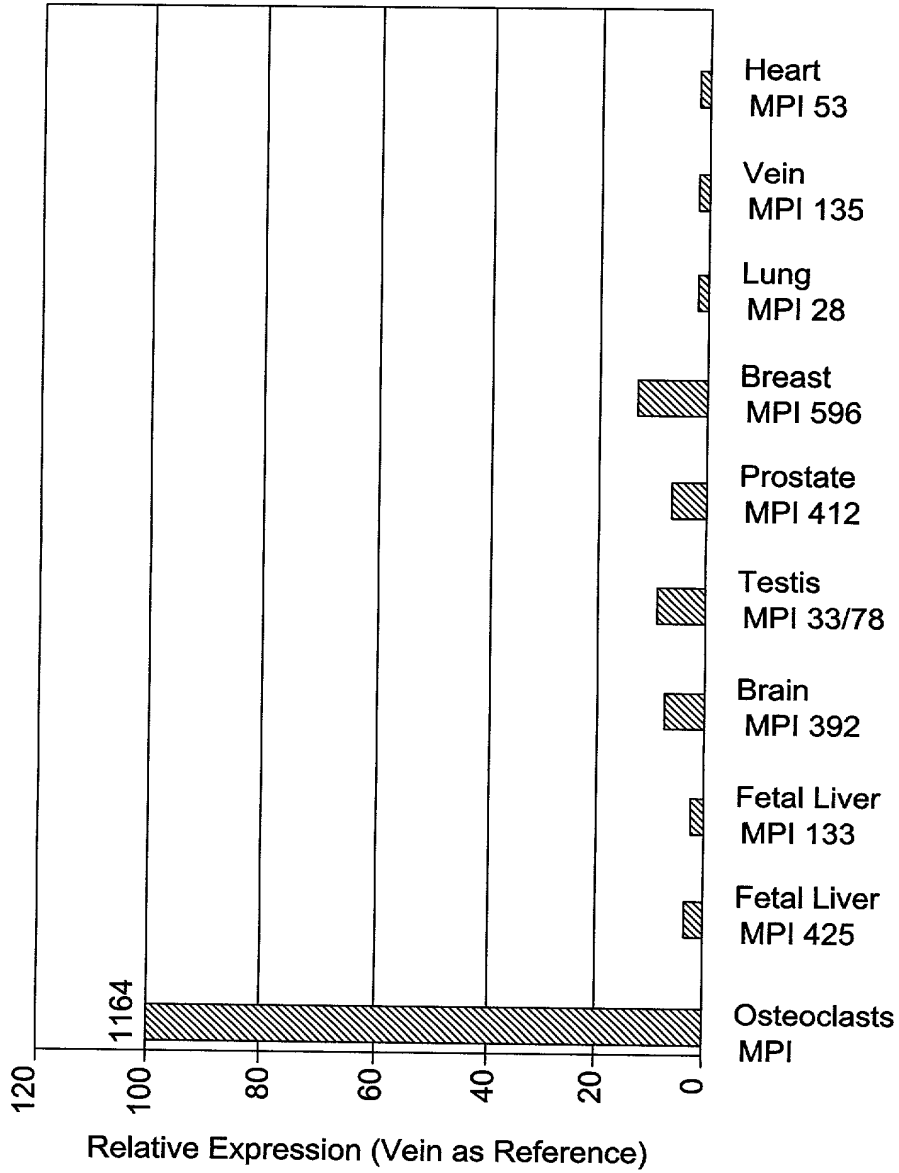


FIG. 8.